

GenCore version 5.1.3
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OM protein - protein search, using SW model
Run on: January 16, 2003, 16:42:17, Search time: 19.713 Seconds
(without alignments)
58.517 Million cell updates/sec

Title: US-09-856-070-21
Perfect score: 60
Sequence: 1 EELMLRLQDYE 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73; *
1: Pir1; *
2: Pir2; *
3: Pir3; *
4: Pir4; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	581	2	ezrin - bovine ezrin (validated)
2	60	100.0	586	1	ezrin - mouse hypothetical prote
3	60	100.0	630	2	ezrin - mouse hypothetical prote
4	57	95.0	586	1	ezrin - mouse hypothetical prote
5	39	65.0	250	2	alpha(1,3)-fucosyl hypothetical prote
6	39	65.0	405	2	alpha(1,3)-fucosyl hypothetical prote
7	39	65.0	884	3	alpha(1,3)-fucosyl hypothetical prote
8	39	65.0	880	2	alpha(1,3)-fucosyl hypothetical prote
9	39	65.0	1263	2	alpha(1,3)-fucosyl hypothetical prote
10	32	64.3	867	2	alpha(1,3)-fucosyl hypothetical prote
11	38	63.3	130	2	alpha(1,3)-fucosyl hypothetical prote
12	38	63.3	150	2	alpha(1,3)-fucosyl hypothetical prote
13	38	63.3	150	2	alpha(1,3)-fucosyl hypothetical prote
14	38	63.3	1058	2	alpha(1,3)-fucosyl hypothetical prote
15	38	63.3	1400	2	alpha(1,3)-fucosyl hypothetical prote
16	37	61.7	111	2	alpha(1,3)-fucosyl hypothetical prote
17	37	61.7	303	1	alpha(1,3)-fucosyl hypothetical prote
18	37	61.7	303	2	alpha(1,3)-fucosyl hypothetical prote
19	37	61.7	306	2	alpha(1,3)-fucosyl hypothetical prote
20	37	61.7	321	2	alpha(1,3)-fucosyl hypothetical prote
21	37	61.7	337	1	alpha(1,3)-fucosyl hypothetical prote
22	37	61.7	454	2	alpha(1,3)-fucosyl hypothetical prote
23	37	61.7	756	2	alpha(1,3)-fucosyl hypothetical prote
24	37	61.7	1305	2	alpha(1,3)-fucosyl hypothetical prote
25	37	61.7	2472	2	alpha(1,3)-fucosyl hypothetical prote
26	37	61.7	2477	1	alpha(1,3)-fucosyl hypothetical prote
27	36	60.0	250	2	alpha(1,3)-fucosyl hypothetical prote
28	36	60.0	294	2	alpha(1,3)-fucosyl hypothetical prote
29	36	60.0	304	2	alpha(1,3)-fucosyl hypothetical prote

ALIGNMENTS									
RESULT 1									
I45889									
ezrin - bovine									
C;Species: Bos primigenius taurus (cattle)									
C;Iso: 15 Oct 1996 #seq-no-c_revise_v15_nov-1996 #text_change 13-Aug-1999									
C;Accession: I45889									
R;Bergon, C M; Zhan, H ; Saich, K ; Duman, R S.; Nestler, E J.									
Mol. Cell. Neurosci. 4: 64-73, 1993									
A;Title: Ezrin and osteocentin, two proteins associated with cell shape and growth, a									
A;Reference Number: 145889									
A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Molecule type:mRNA									
A;Residues: 1-581 									
A;Cross-references: SH:MG8498; NIH:928407; PDB:AAA105101; PID:389408									
C;Superfamily: ezrin; protein: 4.1 membrane-binding domain homology									
F:7-29/1/bovain_EEELMLRLQDYE 12									
Query Match									
Best Local Similarity 100.0%; Score: 60; DB 2; Length 581;									
Matches 12; Conservative 0; Mismatches 0; indels 0; Gaps 0;									
Oy 1 EEELMLRLQDYE 12									
Oy 1 EEELMLRLQDYE 12									
Oy 345 EEELMLRLQDYE 12									
Oy 345 EEELMLRLQDYE 12									
RESULT 2									
A34400									
N;Alternate names: cytoskeletal protein; villin 2									
C;Species: Homo sapiens (human)									
C;CreateDate: 22-Jan-1990 #sequence revision 14-Jul-1994 #text_change 08-Dec-2000									
C;Accession: A34400; S09263; F61002									
P;Paramecium Caudatum; Villin; Villin									
J;Biol. Chem. 264: 16727-16742, 1989									
A;Title: Cytoskeletal filament-associated mRNA sequence, prokaryotic exp									
A;Protein: Villin; AA445; M01296; P04449; P04450; P04451; P04452; P04453; P04454; P04455; P04456; P04457; P04458; P04459; P04460; P04461; P04462; P04463; P04464; P04465; P04466; P04467; P04468; P04469; P04470; P04471; P04472; P04473; P04474; P04475; P04476; P04477; P04478; P04479; P04480; P04481; P04482; P04483; P04484; P04485; P04486; P04487; P04488; P04489; P04490; P04491; P04492; P04493; P04494; P04495; P04496; P04497; P04498; P04499; P04400; P04401; P04402; P04403; P04404; P04405; P04406; P04407; P04408; P04409; P04410; P04411; P04412; P04413; P04414; P04415; P04416; P04417; P04418; P04419; P04420; P04421; P04422; P04423; P04424; P04425; P04426; P04427; P04428; P04429; P04430; P04431; P04432; P04433; P04434; P04435; P04436; P04437; P04438; P04439; P04440; P04441; P04442; P04443; P04444; P04445; P04446; P04447; P04448; P04449; P04450; P04451; P04452; P04453; P04454; P04455; P04456; P04457; P04458; P04459; P04460; P04461; P04462; P04463; P04464; P04465; P04466; P04467; P04468; P04469; 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Species: *Arabidopsis thaliana* (mouse-ear cress); Date: 02 Mar 2001; Sequence revision: 02 Mar 2001; Last update: 31 Mar 2001
 Accession #: E06544
 Authors: Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chinnaiyan, M.K.; Conn, L.; Chee, Y.; Cenay, A.R.; Creasy, T.H.; Guschin, D.; Hirsch, H.; Hochstschild, A.; Huhner, A.; Jorgenson, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Li, J.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lazarus, J.S.; Maiti, P.; Mazzoni, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tackmann, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*. Reference number: A86141; PMID: 11130712

A: Molecule type: DNA	ATU0740	C: Cross-references: GR-ACE017869; PIDN:AAK8648_1; PMID:q15155710; GSPIB:GN00169
A: Cross-references:		
C: Genetics:		
A: Gene: AGR C 1339		
A: Map position: circular chromosome		
C: Superfamily: regulatory protein asnc		
Query Match	63/38;	Score 38; DB 2; Length 150;
Best Local Similarity	80.0%	Pred. No. 17;
Matches	8;	Mismatches 1;
Conservative		Indels 0;
		Gaps 0;
Qy		
3 LMLRLQYEE 12		
Db	106 LMLRLDME 115	
RESULT 13		
ATU0740		
transcription regulator, Asnc family		ATU0740 Imported - <i>Agrobacterium tumefaciens</i>
C: Species: <i>Agrobacterium tumefaciens</i>		
C: Date: 11-Jan-2002 #text_change 01-Feb-2002		
C: Accession: AF2667		
CF: Wood, D.W.; Stetubhai, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.F.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Gaenthaler, D.; Kutayvin, I.; Levy, R.; Li, M.; Karpe, P.; Komar, P.; Zhang, S.		
Science 294, 2317-2324, 2001		
A: Authors: Yoo, H.; Tao, Y.; Biddle, F.; Jand, M.; Krespan, W.; Perry, M.; Gordorster, E.W.		
A: Title: The Genome of the Natural Genetic Engineer <i>Agrobacterium tumefaciens</i> C5		
A: Reference number: AH2577; PMID:11743193		
A: Accession: AF2667		
A: Status: preliminary		
A: Molecule type: DNA		
A: Residues: 1-150 <KDE>		
A: Cross references: GR-AE008688; PIDN:AA41756_1; PMID:q17739108; GSPIB:GN00186		
A: Experimental source: strain C58 (Dupont)		
C: Genetics:		
A: Gene: ATU0740		
A: Map position: circular chromosome		
C: Superfamily: regulatory protein asnc		
Query Match	63/38;	Score 38; DB 2; Length 150;
Best Local Similarity	80.0%	Pred. No. 17;
Matches	8;	Mismatches 1;
Conservative		Indels 0;
		Gaps 0;
Qy		
3 LMLRLQYEE 12		
Db	106 LMLRLDME 115	
RESULT 14		
S65460		
apolipoprotein B - Atlantic salmon (fragment)		
C: Species: Salmo salar (Atlantic salmon)		#text_change 2-Dec-1997
C: Date: 04-Dec-1997 #text_change 2-Dec-1997		
C: Accession: S65460; T51362		
CF: Babio, P.J.; Deryckere, F.; Gannon, F.		
Eur. J. Biochem. 230:45-51, 1995		
A: Title: presence of an extended duplication in the putative low-density lipoprotein receptor gene of Atlantic salmon		
A: Reference number: 151362; PMID:9524549; PMID:7541349		
A: Accession: S65460		
A: Status: nuclear acid sequence not shown		
A: Molecule type: mRNA		
A: Residues: 1-158 - DAB-		
C: Cross references: EMBL:X61856; NM:NM:CAA5744_1; PR:PR:9854619		
A: Experimental source: liver		
C: Genetics:		
A: Gene: apob		
C: Superfamily: apolipoprotein B metabolism; chylomicron; glycoprotein; intestinal macrophage		
Qy		
3 QY 38;		Score 38; DB 2; Length 150;
Db	106 LMLRLDME 115	

Host local Similarity 58.38; Pred. No. 1.3e-02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 EELMLRQDYEE 12
 Db 1013 KETQKIKHDYEE 1024

RESULT 15

T22644 hypothetical protein F54D1.5 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision_15 Oct-1999 #text_change_15-Oct-1999

C;Accession: T22644

R;Leonard, N.

submitted to the EMBL Data Library, July 1996

A;Reference number: 219592

A;Accession: T22644

A;Status: Preliminary, translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1400 <WIL>

A;Cross-references: EMBL:27112, EDDN:CAH05821, ISIPI:G8A522, TESF:154D1.5

A;Experimental source: clone F54D1

C;Genetics

A;Gene: CESP:F54D1.5

A;Map position: 4

A;Introns: 21/2; 51/1; 204/2; 276/1; 464/2; 444/2; 464/4; 533/4; 545/4; 544/4; 572/2; 69

Query Match 63.38; Score 38; DB 2; Length 1400;

Host local Similarity 58.38; Pred. No. 1.8e-02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EELMLRQDYEE 12

Db 1195 EDEMKTQDFEE 1206

Search completed: January 16, 2003, 16:57:51

Job time : 20.7143 secs

